



- 1 -

SEQUENCE LISTING

<110> Luecke, Hartmut
Prosise, Glen

<120> Crystal Structures of T. Foetus Inosine
Monophosphate Dehydrogenase In Complex With Substrate,
CoFactor and Analogs and Uses Thereof

<130> 66778-355

<140> US 10/663,347

<141> 2003-09-15

<150> 60/410,523

<151> 2002-09-13

<150> 60/412,044

<151> 2002-09-18

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 503

<212> PRT

<213> Tritrichomonas foetus

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			20					25					30		
Leu	Ser	Thr	Pro	Leu	Val	Lys	Phe	Gln	Lys	Gly	Gln	Gln	Ser	Glu	Ile
		35					40					45			
Asn	Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly
	50					55					60				
Glu	Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile
65					70					75					80
Phe	Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val
			85						90					95	
Lys	Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro
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Asp	Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His
		115					120					125			
Asn	Thr	Val	Ala	Val	Thr	Asp	Asp	Gly	Thr	Pro	His	Gly	Val	Leu	Leu
	130					135					140				
Gly	Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu
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Thr	Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala

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Leu	Ile	Pro	Gly	Leu	Ser	Thr	Val	Asp	Cys	Ile	Pro	Ser	Asn	Val	Asn
			20					25					30		
Leu	Ser	Thr	Pro	Leu	Val	Lys	Phe	Gln	Lys	Gly	Gln	Gln	Ser	Glu	Ile
		35					40					45			
Asn	Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly
	50					55					60				
Glu	Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile
65					70					75					80
Phe	Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val
				85					90					95	
Lys	Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro
			100					105					110		
Asp	Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His
		115					120					125			
Asn	Thr	Val	Ala	Val	Thr	Asp	Asp	Gly	Thr	Pro	His	Gly	Val	Leu	Leu
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Gly	Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu
145					150					155					160
Thr	Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala
				165					170					175	
His	Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys
			180					185					190		
Lys	Leu	Asn	Ala	Leu	Pro	Ile	Ile	Asp	Asp	Asp	Gln	His	Leu	Arg	Tyr
		195					200					205			
Ile	Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu
	210					215					220				
Leu	Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr
225					230					235					240
Arg	Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp
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Val	Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile
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Thr	Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly
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Ala	Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala
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Gly	Ala	Asp	Phe	Ile	Lys	Ile	Gly	Ile	Gly	Gly	Gly	Ser	Ile	Xaa	Ile
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Thr	Arg	Glu	Gln	Lys	Gly	Ile	Gly	Arg	Gly	Gln	Ala	Thr	Ala	Val	Ile
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Asp	Val	Val	Ala	Glu	Arg	Asn	Lys	Tyr	Phe	Glu	Glu	Thr	Gly	Ile	Tyr
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Ile	Pro	Val	Cys	Ser	Asp	Gly	Gly	Ile	Val	Tyr	Asp	Tyr	His	Met	Thr
		355					360					365			
Leu	Ala	Leu	Ala	Met	Gly	Ala	Asp	Phe	Ile	Met	Leu	Gly	Arg	Tyr	Phe
	370					375					380				
Ala	Arg	Phe	Glu	Glu	Ser	Pro	Thr	Arg	Lys	Val	Thr	Ile	Asn	Gly	Ser
385					390					395					400
Val	Met	Lys	Glu	Tyr	Trp	Gly	Glu	Gly	Ser	Ser	Arg	Ala	Arg	Asn	Trp

[illegible]